

Supplementary Table S10. RNA-sequencing quality parameters.

	mean	(SD)
Total clusters (in millions) ^a	32.3	(1.2)
Total reads (in millions) ^b	64.5	(2.4)
Qual score ^c	36.0	(0.1)
% rRNA ^d	5.6	(1.2)
Number of genes detected	13667	(156)
% Transcriptome mapped ^e	51.8	(1.9)
% All reads mapped ^f	90.9	(1.3)
% Mapped bases		
'A'	22.7	(0.3)
'C'	25.7	(0.3)
'G'	25.3	(0.3)
'T'	26.3	(0.4)
Reads aligned to transcriptome (in millions) ^g	33.0	(1.8)
% Alignment to transcriptome ^h	51.1	(1.9)
Mapped reads (in millions) ⁱ	72.9	(2.8)
% Reads aligned ^j	91.8	(1.3)
Total alignments (in millions) ^k	63.8	(3.1)
Mean mapping quality ^l	170.8	(5.3)
Mean read length (bp) ^m	50.9	(0.0)

^a Total clusters: Number of reads in the library -- prealignment

^b Number of reads: Total reads for this sample -- postalignment

^c Qual score: Average read quality (reads 1 and 2)

^d % rRNA: Percent of reads aligning to ribosomal RNAs

^e % Transcriptome mapped: Percentage of reads that are mapped to the transcriptome

^f % All reads mapped: Percent of reads mapped either to the transcriptome or the genome

^g Reads aligned to transcriptome: The number of reads aligned to the transcriptome

^h Percent alignment to transcriptome: The percent of reads aligned to the transcriptome

^{i-m} Statistics representing a combination of alignment to the transcriptome and subsequent alignment to the genome

ⁱ Mapped reads: The number of reads aligned to either the transcriptome or the genome

^j % Reads aligned: The percent of reads aligned to the transcriptome or the genome

^j Total alignments: Total number of alignments, including ambiguous ones

^l Mean mapping quality: A measure of how well a read aligned to the sequence. This is a mean of those quality values; subject to skewing because of ambiguous reads.

^m Mean read length: The average read length, typically shorter than the max because of sequence clipping